



SEQUENCE LISTING

<110> Bandaru, Rajasekhar

<120> 68730 and 69112, Protein Kinase
Molecules and Uses Therefor

<130> MPI2000-521P1R(M)

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<141> 2001-12-17

<150> 60/258222

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gag aac ggc gag agc agc tcc tcc tgg aaa aag caa gct gaa gac atc 225

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gaa	gtg	gtt	tta	gct	gaa	gag	aag	gca	act	ggc	aag	ctc	ttt	gct	gtg	321
Glu	Val	Val	Leu	Ala	Glu	Glu	Lys	Ala	Thr	Gly	Lys	Leu	Phe	Ala	Val	
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Lys	Cys	Ile	Pro	Lys	Lys	Ala	Leu	Lys	Gly	Lys	Glu	Ser	Ser	Ile	Glu	
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Asn	Glu	Ile	Ala	Val	Leu	Arg	Lys	Ile	Lys	His	Glu	Asn	Ile	Val	Ala	
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ctg	gtg	tcc	ggt	gga	gag	ctg	ttt	gac	cg	ata	gtg	gag	aag	ggg	ttt	513
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Tyr	Thr	Glu	Lys	Asp	Ala	Ser	Thr	Leu	Ile	Arg	Gln	Val	Leu	Asp	Ala	
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Ser	Asp	Phe	Gly	Leu	Ser	Lys	Met	Glu	Gly	Lys	Gly	Asp	Val	Met	Ser	
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245

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His Pro Trp Ile Ala Gly Asp Thr Ala Leu Asn Lys Asn Ile His Glu	
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Ser Val Ser Ala Gln Ile Arg Lys Asn Phe Ala Lys Ser Lys Trp Arg	
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Met Gly Lys Glu Pro Leu Thr Leu Lys Ser Ile Gln Val

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Gln His Ser Arg Ala Pro Ser Pro Arg Leu Arg Ser Arg Leu Phe Ser
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Ser Cys Ser Glu Val Ala Gly Cys Lys Ala Ala Met Arg His Gln Gly
65 70 75

aag atc ccc gag gag ctt tca cta gat gac aga gcg agg acc cag aag 1491
Lys Ile Pro Glu Glu Leu Ser Leu Asp Asp Arg Ala Arg Thr Gln Lys
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Lys Trp Gly Arg Gly Lys Trp Glu Pro Glu Pro Ser Ser Lys Pro Pro
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Cys Lys Arg Glu Arg Glu Leu Gln Gln Ser Leu Glu Arg Glu Arg Leu		
145	150	155
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175	180	185
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Gly Ala Ala Lys Ala Lys Lys Asp Leu Val Glu Val Leu Pro Val Thr		
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Glu Glu Gly Leu Arg Glu Val Lys Lys Asp Thr Arg Pro Met Ser Arg		
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Pro Ala Lys Leu Glu Lys Glu Pro Lys Thr Arg Pro Glu Glu Asn Lys		
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Pro Glu Arg Pro Ser Gly Arg Lys Pro Arg Pro Met Gly Ile Ile Ala		
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Ala Asn Val Glu Lys His Tyr Glu Thr Gly Arg Val Ile Gly Asp Gly			
350	355	360	365
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Tyr Ala Met Lys Ile Ile Asp Lys Ser Arg Leu Lys Gly Lys Glu Asp			
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Ser Val Lys Phe Pro Glu Pro Asp Ala Ala Leu Met Ile Met Asp Leu			
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Cys Lys Ala Leu Val His Met His Asp Lys Ser Ile Val His Arg Asp			
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Leu Lys Pro Glu Asn Leu Val Gln Arg Asn Glu Asp Lys Ser Thr			
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Ile Leu Tyr Ile Leu Leu Cys Gly Phe Pro Pro Phe Arg Ser Pro Glu			
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575	580	585	
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Val Ser Arg Leu Leu Val Val Asp Pro Lys Lys Arg Tyr Thr Ala His			

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Arg Gly Lys Trp Glu Pro Glu Pro Ser Ser Lys Pro Pro Arg Glu Ala															
100	105	110													
Thr Leu Glu Glu Arg His Ala Arg Gly Glu Lys His Leu Gly Val Glu															
115	120	125													
Ile Glu Lys Thr Ser Gly Glu Ile Ile Arg Cys Glu Lys Cys Lys Arg															
130	135	140													
Glu Arg Glu Leu Gln Gln Ser Leu Glu Arg Glu Arg Leu Ser Leu Gly															
145	150	155	160												
Thr Ser Glu Leu Asp Met Gly Lys Gly Pro Met Tyr Asp Val Glu Lys															
165	170	175													
Leu Val Arg Thr Arg Ser Cys Arg Arg Ser Pro Glu Ala Asn Pro Ala															
180	185	190													
Ser Gly Glu Glu Gly Trp Lys Gly Asp Ser His Arg Ser Ser Pro Arg															
195	200	205													
Asn Pro Thr Gln Glu Leu Arg Arg Pro Ser Lys Ser Met Asp Lys Lys															
210	215	220													
Glu Asp Arg Gly Pro Glu Asp Gln Glu Ser His Ala Gln Gly Ala Ala															
225	230	235	240												
Lys Ala Lys Lys Asp Leu Val Glu Val Leu Pro Val Thr Glu Glu Gly															
245	250	255													
Leu Arg Glu Val Lys Lys Asp Thr Arg Pro Met Ser Arg Ser Lys His															

260	265	270
Gly	Gly	
Trp	Leu	Arg
Leu	Arg	Glu
	His	Gln
	Ala	Gly
	Phe	Glu
	Lys	Leu
	Arg	Arg
Arg	Thr	Gly
	Glu	Glu
	Lys	Glu
	Ala	Glu
	Lys	Glu
	Lys	Lys
	Pro	Cys
275	280	285
290	295	300
Met	Ser	Gly
Gly	Arg	Arg
Arg	Arg	Met
Met	Thr	Leu
	Arg	Asp
	Asp	Gln
	Pro	Ala
		Lys
305	310	315
320		
Leu	Glu	Lys
Glu	Pro	Lys
Pro	Thr	Arg
Glu	Pro	Glu
Glu	Asn	Lys
Lys	Pro	Glu
	Arg	
325	330	335
335		
Pro	Ser	Gly
Gly	Arg	Lys
Arg	Pro	Pro
Pro	Met	Gly
Met	Ile	Ile
	Ala	Ala
	Asn	Val
340	345	350
350		
Glu	Lys	His
Tyr	Glu	Thr
Gly	Arg	Val
Arg	Ile	Gly
Asp	Gly	Asp
355	360	365
365		
Val	Val	Lys
Glu	Cys	Arg
Arg	His	Arg
Glu	Thr	Arg
Thr	Arg	Gln
Gln	Ala	Tyr
Ala	Tyr	Ala
		Met
370	375	380
380		
Lys	Ile	Ile
Asp	Lys	Ser
Ser	Arg	Leu
Leu	Lys	Gly
		Lys
		Glu
385	390	395
400		
Ser	Glu	Ile
Ile	Leu	Ile
Ile	Gln	Ser
Leu	Ser	His
		Pro
		Asn
		Ile
		Val
		Lys
405	410	415
415		
Leu	His	Glu
His	Val	Tyr
Tyr	Glu	Thr
Asp	Met	Glu
		Ile
		Tyr
		Leu
		Ile
		Glu
420	425	430
430		
Tyr	Val	Gln
Gly	Gly	Asp
Asp	Leu	Phe
Phe	Asp	Ala
Ala	Ile	Ile
		Glu
		Ser
		Val
		Lys
435	440	445
445		
Phe	Pro	Glu
Pro	Asp	Ala
Asp	Ala	Leu
Leu	Met	Ile
		Met
		Asp
		Leu
		Cys
		Lys
450	455	460
460		
Leu	Val	His
His	Asp	Ser
Ser	Ile	Val
Val	His	Arg
Arg	Asp	Asp
Asp	Leu	Lys
		Pro
		Leu
		Lys
465	470	475
480		
Glu	Asn	Leu
Leu	Leu	Val
		Gln
		Arg
		Asn
		Glu
		Asp
		Lys
485	490	495
495		
Leu	Ala	Asp
Asp	Phe	Gly
Gly	Leu	Ala
Ala	Lys	His
		Val
		Val
		Arg
		Pro
		Ile
		Phe
500	505	510
510		
Val	Cys	Gly
Gly	Thr	Pro
Pro	Thr	Tyr
Tyr	Val	Ala
Ala	Pro	Glu
Glu	Ile	Leu
Leu	Ser	Glu
		Lys
515	520	525
525		
Gly	Tyr	Leu
Leu	Glu	Val
		Asp
		Met
		Trp
		Ala
		Ala
		Gly
		Val
		Ile
		Leu
		Tyr
530	535	540
540		
Ile	Leu	Cys
Cys	Gly	Phe
Phe	Pro	Pro
Pro	Phe	Arg
Arg	Ser	Pro
Pro	Glu	Arg
Glu	Ile	Asp
Asp	Ile	Ile
Ile	Gln	Leu
Leu	Gly	His
		Phe
		Glu
		Phe
		Leu
		Pro
545	550	555
560		
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Glu	Phe	Asn
Asn	Ile	Ile
Ile	Gln	Leu
Leu	Gly	His
		Phe
		Glu
		Phe
		Leu
565	570	575
575		
Pro	Tyr	Trp
Trp	Asp	Asn
Asn	Ile	Ser
Ser	Asp	Ala
Ala	Ala	Lys
		Asp
		Leu
		Val
		Ser
580	585	590
590		
Leu	Leu	Val
Val	Val	Asp
		Pro
		Lys
		Arg
		Tyr
		Thr
		Ala
		His
		Gln
595	600	605
605		
Gln	His	Pro
Pro	Trp	Ile
Ile	Glu	Thr
Thr	Ala	Gly
Gly	Lys	Thr
Thr	Asn	Thr
Asn	Thr	Val
Val	Lys	Arg
610	615	620
620		
Gln	Lys	Gln
Gln	Val	Ser
Val	Ser	Pro
Pro	Ser	Ser
Ser	Glu	Gly
Gly	His	Phe
Phe	Arg	Ser
Ser	Gln	His
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Lys	Arg	Val
Val	Val	Glu
Gln	Val	Ser
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<211> 1947

<212> DNA

<213> Homo sapiens

<400> 6

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 aagagctgca gcgaagtgc aggatgcaag gcagccatga ggcaccaggc gaagatcccc 240

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<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus sequence involved in ATP binding
(Prosite Accession No. PS00107)

<221> VARIANT

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<223> Leu can be Ile or Val.

<221> VARIANT

<222> 3

<223> Xaa can be any amino acid except Pro.

<221> VARIANT

<222> 5

<223> Xaa can be any amino acid except Pro.

<221> VARIANT

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<223> Phe can be Tyr, Trp, Met, Gly, Ser, Thr, Asn, or His.

<221> VARIANT

<222> 7

<223> Ser can be Gly or Ala.

<221> VARIANT

<222> (8)...(8)
<223> Xaa can be any amino acid except Pro or Trp.

<221> VARIANT
<222> (9)...(9)
<223> Leu can be Ile, Val, Cys, Ala, or Thr.

<221> VARIANT
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<223> Xaa can be any amino acid except Pro or Asp.

<221> VARIANT
<222> (11)...(11)
<223> Xaa can be any amino acid.

<221> VARIANT
<222> (12)...(12)
<223> Gly can be Ser, Thr, Ala, Cys, Leu, Ile, Val, Met, Phe, or Tyr.

<221> VARIANT
<222> (13)...(13)
<223> Xaa can be any amino acid and asfew as 5 and as many as 18 amino acids.

<221> VARIANT
<222> (14)...(14)
<223> Leu can be Ile, Val, Met, Phe, Tyr, Trp, Cys, Ser, Thr, Ala, or Arg.

<221> VARIANT
<222> (15)...(15)
<223> Ala can be Ile, Val, or Pro.

<221> VARIANT
<222> (16)...(16)
<223> Leu can be Ile, Val, Met, Phe, Ala, Gly, Cys. Lys, or Arg.

<221> BINDING
<222> (17)...(17)

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1 5 10 15
Lys

<210> 8
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence for serine/threonine kinases
(Prosite Accession No. PS00108)

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<223> Leu can be Ile, Val, Met, Phe, or Tyr

<221> VARIANT
<222> 2
<223> Xaa can be any amino acid.

<221> VARIANT
<222> 3
<223> His can be Tyr.

<221> VARIANT
<222> 4
<223> Xaa can be any amino acid.

<221> ACT_SITE
<222> 5

<221> VARIANT
<222> (6)...(6)
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<221> VARIANT
<222> (8)...(9)
<223> Xaa can be any amino acid.

<221> VARIANT
<222> (11)...(11)
<223> Leu can be Ile, Val, Met, Phe, Tyr, Cys, or Thr.

<221> VARIANT
<222> (12)...(12)
<223> Leu can be Ile, Val, Met, Phe, Tyr, Cys, or Thr.

<221> VARIANT
<222> (13)...(13)
<223> Leu can be Ile, Val, Met, Phe, Tyr, Cys, or Thr.

<400> 8
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<210> 9
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<212> PRT
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<220>
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Accession No. PS00109;

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<221> VARIANT
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<223> Xaa can be any amino acid.

<221> VARIANT
<222> 3

<223> His can be Tyr.

<221> VARIANT

<222> 4

<223> Xaa can be any amino acid.

<221> ACT_SITE

<222> 5

<221> VARIANT

<222> (6)...(6)

<223> Leu can be Ile, Val, Met, Phe, or Tyr.

<221> VARIANT

<222> (7)...(7)

<223> Arg can be Ser, Thr, Ala, or Cys.

<221> VARIANT

<222> (8)...(9)

<223> Xaa can be any amino acid.

<221> VARIANT

<222> (11)...(11)

<223> Leu can be Ile, Val, Met, Phe, Tyr, or Cys.

<221> VARIANT

<222> (12)...(12)

<223> Leu can be Ile, Val, Met, Phe, Tyr, or Cys.

<221> VARIANT

<222> (13)...(13)

<223> Leu can be Ile, Val, Met, Phe, Tyr, or Cys.

<400> 9

Leu Xaa His Xaa Asp Leu Arg Xaa Xaa Asn Leu Leu Leu

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5

10

<210> 10

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus Sequence for tyrosine kinase
phosphorylation site (Prosite Accession No.
PS00007)

<221> VARIANT

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<223> Arg can be Lys.

<221> VARIANT

<222> 2

<223> Xaa can be any amino acid and can be two or three
amino acids

<221> VARIANT

<222> 3

<223> Asp can be Glu.

<221> VARIANT
<222> 4
<223> Xaa can be any amino acid and can be two or three
amino acids

<221> PHOSPHORYLATION
<222> 5

<400> 10
Arg Xaa Asp Xaa Tyr
1 5